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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/954,936

DATE: 01/07/2002

TIME: 14:47:57

Input Set : N:\Crf3\RULE60\09954936.raw

Output Set: N:\CRF3\01072002\I954936.raw

ENTERED

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1 <110> APPLICANT: Briggs, Clark A.
2   Gopalakrishnan, Murali
3   McKenna, David G.
4   Monteggia, Lisa M.
5   Roch, Jean-Marc
6   Sullivan, James P.
7   Touma, Edward
8   Abbott Laboratories
9 <120> TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
10  RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
11 <130> FILE REFERENCE: 6017.US.01
12 <140> CURRENT APPLICATION NUMBER: 09/954,936
13 <141> CURRENT FILING DATE: 2001-09-18
14 <150> PRIOR APPLICATION NUMBER: 08/771,737
15 <151> PRIOR FILING DATE: 1996-12-20
16 <160> NUMBER OF SEQ ID NOS: 8
17 <170> SOFTWARE: FastSEQ for Windows Version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1590
21 <212> TYPE: DNA
22 <213> ORGANISM: homo sapien
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (9)...(1514)
26 <400> SEQUENCE: 1
27   tcgagccc atg agg tgt agc ccc gga gga gtg tgg ctg gca ctg gca gca      50
28       Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala
29       1             5             10
30   tct ctc ctg cac gtg tcc ctg caa ggc gag ttc cag agg aag ctt tac      98
31   Ser Leu Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr
32   15             20             25             30
33   aag gag ctg gtc aag aac tac aat ccc ttg gag agg ccc gtg gcc aat      146
34   Lys Glu Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn
35   35             40             45
36   gac tcg caa cca ctc acc gtc tac ttc tcc ctg agc ctc ctg cag atc      194
37   Asp Ser Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile
38   50             55             60
39   atg gac gtg gat gag aag aac caa gtt tta acc acc aac att tgg ctg      242
40   Met Asp Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu
41   65             70             75
42   caa atg tct tgg aca gat cac tat tta cag tgg aat gtg tca gaa tat      290
43   Gln Met Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr
44   80             85             90
45   cca ggg gtg aag act gtt cgt ttc cca gat ggc cag att tgg aaa cca      338
46   Pro Gly Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro
47   95             100            105            110
48   gac att ctt ctc tat aac agt gct gat gag cgc ttt gac gcc aca ttc      386

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49	Asp	Ile	Leu	Leu	Tyr	Asn	Ser	Ala	Asp	Glu	Arg	Phe	Asp	Ala	Thr	Phe	
50					115					120					125		
51	cac	act	aac	gtg	ttg	gtg	aat	tct	tct	ggg	cat	tgc	cag	tac	ctg	cct	434
52	His	Thr	Asn	Val	Leu	Val	Asn	Ser	Ser	Gly	His	Cys	Gln	Tyr	Leu	Pro	
53				130						135					140		
54	cca	ggc	ata	ttc	aag	agt	tcc	tgc	tac	atc	gat	gta	cgc	tgg	ttt	ccc	482
55	Pro	Gly	Ile	Phe	Lys	Ser	Ser	Cys	Tyr	Ile	Asp	Val	Arg	Trp	Phe	Pro	
56			145						150						155		
57	ttt	gat	gtg	cag	cac	tgc	aaa	ctg	aag	ttt	ggg	tcc	tgg	tct	tac	gga	530
58	Phe	Asp	Val	Gln	His	Cys	Lys	Leu	Lys	Phe	Gly	Ser	Trp	Ser	Tyr	Gly	
59		160					165				170						
60	ggc	tgg	tcc	ttg	gat	ctg	cag	atg	cag	gag	gca	gat	atc	agt	ggc	tat	578
61	Gly	Trp	Ser	Leu	Asp	Leu	Gln	Met	Gln	Glu	Ala	Asp	Ile	Ser	Gly	Tyr	
62		175				180				185						190	
63	atc	ccc	aat	gga	gaa	tgg	gac	cta	gtg	gga	atc	ccc	ggc	aag	agg	agt	626
64	Ile	Pro	Asn	Gly	Glu	Trp	Asp	Leu	Val	Gly	Ile	Pro	Gly	Lys	Arg	Ser	
65			195							200					205		
66	gaa	agg	ttc	tat	gag	tgc	tgc	aaa	gag	ccc	tac	ccc	gat	gtc	acc	ttc	674
67	Glu	Arg	Phe	Tyr	Glu	Cys	Cys	Lys	Glu	Pro	Tyr	Pro	Asp	Val	Thr	Phe	
68			210						215					220			
69	aca	gtg	acc	atg	cgc	cgc	agg	aca	ctc	tac	tat	ggc	ctc	aac	ctg	ctg	722
70	Thr	Val	Thr	Met	Arg	Arg	Arg	Thr	Leu	Tyr	Tyr	Gly	Leu	Asn	Leu	Leu	
71			225					230					235				
72	atc	ccc	tgt	gtg	ctc	atc	tcc	gcc	ctc	gcc	ctg	ctg	gtg	ttc	ctg	ctt	770
73	Ile	Pro	Cys	Val	Leu	Ile	Ser	Ala	Leu	Ala	Leu	Leu	Val	Phe	Leu	Leu	
74		240					245					250					
75	cct	gca	gat	tcc	ggg	gag	aag	att	tcc	ctg	ggg	ata	aca	gtc	tta	ctc	818
76	Pro	Ala	Asp	Ser	Gly	Glu	Lys	Ile	Ser	Leu	Gly	Ile	Thr	Val	Leu	Leu	
77		255			260						265				270		
78	tct	ctt	acc	acc	ttc	atg	ctg	ctc	gtg	gct	gag	atc	atg	ccc	gca	aca	866
79	Ser	Leu	Thr	Thr	Phe	Met	Leu	Leu	Val	Ala	Glu	Ile	Met	Pro	Ala	Thr	
80			275						280					285			
81	tcc	gat	tcg	gta	cca	ttg	ata	gcc	cag	tac	ttc	gcc	agc	acc	atg	atc	914
82	Ser	Asp	Ser	Val	Pro	Leu	Ile	Ala	Gln	Tyr	Phe	Ala	Ser	Thr	Met	Ile	
83			290					295					300				
84	atc	gtg	ggc	ctc	tcg	gtg	gtg	gtg	acg	gtg	atc	gtg	ctg	cag	tac	cac	962
85	Ile	Val	Gly	Leu	Ser	Val	Val	Val	Thr	Val	Ile	Val	Leu	Gln	Tyr	His	
86		305					310					315					
87	cac	cac	gac	ccc	gac	ggc	ggc	aag	atg	ccc	aag	tgg	acc	aga	gtc	atc	1010
88	His	His	Asp	Pro	Asp	Gly	Gly	Lys	Met	Pro	Lys	Trp	Thr	Arg	Val	Ile	
89		320					325					330					
90	ctt	ctg	aac	tgg	tgc	gcg	tgg	ttc	ctg	cga	atg	aag	agg	ccc	ggg	gag	1058
91	Leu	Leu	Asn	Trp	Cys	Ala	Trp	Phe	Leu	Arg	Met	Lys	Arg	Pro	Gly	Glu	
92		335				340				345					350		
93	gac	aag	gtg	cgc	ccg	gcc	tgc	cag	cac	aag	cag	cgg	cgc	tgc	agc	ctg	1106
94	Asp	Lys	Val	Arg	Pro	Ala	Cys	Gln	His	Lys	Gln	Arg	Arg	Cys	Ser	Leu	
95			355							360				365			
96	gcc	agt	gtg	gag	atg	agc	gcc	gtg	gcg	ccg	ccg	ccc	gcc	agc	aac	ggg	1154
97	Ala	Ser	Val	Glu	Met	Ser	Ala	Val	Ala	Pro	Pro	Pro	Ala	Ser	Asn	Gly	

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98          370          375          380
99 aac ctg ctg tac atc ggc ttc cgc ggc ctg gac ggc gtg cac tgt gtc 1202
100 Asn Leu Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val
101          385          390          395
102 ccg acc ccc gac tct ggg gta gtg tgt ggc cgc atg gcc tgc tcc ccc 1250
103 Pro Thr Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro
104          400          405          410
105 acg cac gat gag cac ctc ctg cac ggc ggg caa ccc ccc gag ggg gac 1298
106 Thr His Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp
107          415          420          425          430
108 ccg gac ttg gcc aag atc ctg gag gag gtc cgc tac att gcc aac cgc 1346
109 Pro Asp Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg
110          435          440          445
111 ttc cgc tgc cag gac gaa agc gag gcg gtc tgc agc gag tgg aag ttc 1394
112 Phe Arg Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe
113          450          455          460
114 gcc gcc tgt gtg gtg gac cgc ctg tgc ctc atg gcc ttc tcg gtc ttc 1442
115 Ala Ala Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe
116          465          470          475
117 acc atc atc tgc acc atc ggc atc ctg atg tcg gct ccc aac ttc gtg 1490
118 Thr Ile Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val
119          480          485          490
120 gag gcc gtg tcc aaa gac ttt gcg taaccacgcc tggttctgta catgtggaaa 1544
121 Glu Ala Val Ser Lys Asp Phe Ala
122          495          500
123 actcacagat gggcaagcgc tttggcttgg cgagattcgg ccggaa 1590
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 502
127 <212> TYPE: PRT
128 <213> ORGANISM: homo sapien
129 <400> SEQUENCE: 2
130 Met Arg Cys Ser Pro Gly Gly Val Trp Leu Ala Leu Ala Ala Ser Leu
131 1 5 10 15
132 Leu His Val Ser Leu Gln Gly Glu Phe Gln Arg Lys Leu Tyr Lys Glu
133 20 25 30
134 Leu Val Lys Asn Tyr Asn Pro Leu Glu Arg Pro Val Ala Asn Asp Ser
135 35 40 45
136 Gln Pro Leu Thr Val Tyr Phe Ser Leu Ser Leu Leu Gln Ile Met Asp
137 50 55 60
138 Val Asp Glu Lys Asn Gln Val Leu Thr Thr Asn Ile Trp Leu Gln Met
139 65 70 75 80
140 Ser Trp Thr Asp His Tyr Leu Gln Trp Asn Val Ser Glu Tyr Pro Gly
141 85 90 95
142 Val Lys Thr Val Arg Phe Pro Asp Gly Gln Ile Trp Lys Pro Asp Ile
143 100 105 110
144 Leu Leu Tyr Asn Ser Ala Asp Glu Arg Phe Asp Ala Thr Phe His Thr
145 115 120 125
146 Asn Val Leu Val Asn Ser Ser Gly His Cys Gln Tyr Leu Pro Pro Gly
147 130 135 140

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148   Ile Phe Lys Ser Ser Cys Tyr Ile Asp Val Arg Trp Phe Pro Phe Asp
149   145                               150                               155                               160
150   Val Gln His Cys Lys Leu Lys Phe Gly Ser Trp Ser Tyr Gly Gly Trp
151   151                               165                               170                               175
152   Ser Leu Asp Leu Gln Met Gln Glu Ala Asp Ile Ser Gly Tyr Ile Pro
153   153                               180                               185                               190
154   Asn Gly Glu Trp Asp Leu Val Gly Ile Pro Gly Lys Arg Ser Glu Arg
155   155                               195                               200                               205
156   Phe Tyr Glu Cys Cys Lys Glu Pro Tyr Pro Asp Val Thr Phe Thr Val
157   157                               210                               215                               220
158   Thr Met Arg Arg Arg Thr Leu Tyr Tyr Gly Leu Asn Leu Leu Ile Pro
159   159                               225                               230                               235                               240
160   Cys Val Leu Ile Ser Ala Leu Ala Leu Leu Val Phe Leu Leu Pro Ala
161   161                               245                               250                               255
162   Asp Ser Gly Glu Lys Ile Ser Leu Gly Ile Thr Val Leu Leu Ser Leu
163   163                               260                               265                               270
164   Thr Thr Phe Met Leu Leu Val Ala Glu Ile Met Pro Ala Thr Ser Asp
165   165                               275                               280                               285
166   Ser Val Pro Leu Ile Ala Gln Tyr Phe Ala Ser Thr Met Ile Ile Val
167   167                               290                               295                               300
168   Gly Leu Ser Val Val Val Thr Val Ile Val Leu Gln Tyr His His His
169   169                               305                               310                               315                               320
170   Asp Pro Asp Gly Gly Lys Met Pro Lys Trp Thr Arg Val Ile Leu Leu
171   171                               325                               330                               335
172   Asn Trp Cys Ala Trp Phe Leu Arg Met Lys Arg Pro Gly Glu Asp Lys
173   173                               340                               345                               350
174   Val Arg Pro Ala Cys Gln His Lys Gln Arg Arg Cys Ser Leu Ala Ser
175   175                               355                               360                               365
176   Val Glu Met Ser Ala Val Ala Pro Pro Pro Ala Ser Asn Gly Asn Leu
177   177                               370                               375                               380
178   Leu Tyr Ile Gly Phe Arg Gly Leu Asp Gly Val His Cys Val Pro Thr
179   179                               385                               390                               395                               400
180   Pro Asp Ser Gly Val Val Cys Gly Arg Met Ala Cys Ser Pro Thr His
181   181                               405                               410                               415
182   Asp Glu His Leu Leu His Gly Gly Gln Pro Pro Glu Gly Asp Pro Asp
183   183                               420                               425                               430
184   Leu Ala Lys Ile Leu Glu Glu Val Arg Tyr Ile Ala Asn Arg Phe Arg
185   185                               435                               440                               445
186   Cys Gln Asp Glu Ser Glu Ala Val Cys Ser Glu Trp Lys Phe Ala Ala
187   187                               450                               455                               460
188   Cys Val Val Asp Arg Leu Cys Leu Met Ala Phe Ser Val Phe Thr Ile
189   189                               465                               470                               475                               480
190   Ile Cys Thr Ile Gly Ile Leu Met Ser Ala Pro Asn Phe Val Glu Ala
191   191                               485                               490                               495
192   Val Ser Lys Asp Phe Ala
193   193                               500
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 20
197 <212> TYPE: DNA

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Output Set: N:\CRF3\01072002\I954936.raw

198 <213> ORGANISM: Homo Sapien	
199 <400> SEQUENCE: 3	
200 gtttgggtcc tgggtttacg	20
202 <210> SEQ ID NO: 4	
203 <211> LENGTH: 23	
204 <212> TYPE: DNA	
205 <213> ORGANISM: Homo Sapien	
206 <400> SEQUENCE: 4	
207 gcagcatgaa ggtggttaaga gag	23
209 <210> SEQ ID NO: 5	
210 <211> LENGTH: 23	
211 <212> TYPE: DNA	
212 <213> ORGANISM: Homo Sapien	
213 <400> SEQUENCE: 5	
214 ctctcttacc accttcatgc tgc	23
216 <210> SEQ ID NO: 6	
217 <211> LENGTH: 20	
218 <212> TYPE: DNA	
219 <213> ORGANISM: Homo Sapien	
220 <400> SEQUENCE: 6	
221 gtactgcagc acgatcacccg	20
223 <210> SEQ ID NO: 7	
224 <211> LENGTH: 20	
225 <212> TYPE: DNA	
226 <213> ORGANISM: Homo Sapein	
227 <400> SEQUENCE: 7	
228 cgagcccatg aggtgtagcc	20
230 <210> SEQ ID NO: 8	
231 <211> LENGTH: 20	
232 <212> TYPE: DNA	
233 <213> ORGANISM: Homo Sapien	
234 <400> SEQUENCE: 8	
235 ccaggcattc ggagcttgcc	20

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09954936.raw

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